

Genome version 4.5  
 February 1998 - 1998 Database 0.33

CM provided: 11:30:53 AM, 01/27/2000

Run on: January 21, 2000, 18:06:53 : Search time 11.63 Seconds  
 (without alignments)  
 66,766 Million cell updates/sec

Title: US-09-386-591-50

Perfect score: 136

Sequence: 1 LNC01106MF5P9H1:VFLEDS 26

Scoring table: BLOSUM62

Search: 42229 seqs, 2091277 words

Database: SwissProt\_38:\*

Word size: 0

Number of hits: 1 that first two +length: 2 22229

Prod. No. is the number of results produced by change to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

# SUMMARIES

Result No	Score	Query Match	Length	Prod. No.	Ident
1	136	100.0	497	1	CEP2_PABIT
2	117	80.0	493	1	CEP2_HUMAN
3	117	80.0	493	1	CEP2_MOUSE
4	114	81.8	289	1	CEP2_MESAU
5	48	35.3	313	1	YDAD_HAFIN
6	46	33.6	311	1	YDAD_ECOLI
7	45	33.1	673	1	YDAD_HUMAN
8	45	33.1	1699	1	YDAD_HUMAN
9	44	32.4	349	1	ABWD_MOUSE
10	44	32.4	317	1	ABWD_MOUSE
11	44	32.4	317	1	ABWD_MOUSE
12	43	32.0	782	1	ABWD_MOUSE
13	43	32.0	454	1	ABWD_MOUSE
14	43	31.6	212	1	ABWD_MOUSE
15	42	31.2	777	1	ABWD_MOUSE
16	42	30.9	123	1	ABWD_MOUSE
17	42	30.9	227	1	ABWD_MOUSE
18	41	30.5	1245	1	ABWD_MOUSE
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22	41	30.1	607	1	ABWD_MOUSE
23	41	30.1	1013	1	ABWD_MOUSE
24	41	30.1	1147	1	ABWD_MOUSE
25	41	30.1	1147	1	ABWD_MOUSE
26	41	30.1	1147	1	ABWD_MOUSE
27	41	30.1	664	1	ABWD_MOUSE
28	41	30.1	703	1	ABWD_MOUSE
29	41	30.1	635	1	ABWD_MOUSE
30	41	30.1	635	1	ABWD_MOUSE
31	40	29.8	1773	1	ABWD_MOUSE
32	40	29.8	1655	1	ABWD_MOUSE
33	40	29.8	1655	1	ABWD_MOUSE
34	40	29.4	590	1	ABWD_MOUSE
35	40	29.4	379	1	ABWD_MOUSE
36	40	29.4	1996	1	ABWD_MOUSE
37	40	29.4	479	1	ABWD_MOUSE
38	40	29.4	613	1	ABWD_MOUSE
39	40	29.4	346	1	ABWD_MOUSE

Ident: 1  
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 44 32.4 349 1 ABWD\_MOUSE  
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## ALIGNMENTS

Result	1	Query Match	Score	DB 1	Length	Prod. No.
CEP2_PABIT	136	100.0%	136	DB 1	Length 497	
1	136	100.0%	136	DB 1	Length 497	
2	117	80.0%	117	DB 1	Length 493	
3	117	80.0%	117	DB 1	Length 493	
4	114	81.8%	114	DB 1	Length 289	
5	48	35.3%	48	DB 1	Length 313	
6	46	33.6%	46	DB 1	Length 311	
7	45	33.1%	45	DB 1	Length 673	
8	45	33.1%	45	DB 1	Length 1699	
9	44	32.4%	44	DB 1	Length 349	
10	44	32.4%	44	DB 1	Length 317	
11	44	32.4%	44	DB 1	Length 317	
12	43	32.0%	43	DB 1	Length 782	
13	43	32.0%	43	DB 1	Length 454	
14	43	31.6%	43	DB 1	Length 212	
15	42	31.2%	42	DB 1	Length 777	
16	42	30.9%	42	DB 1	Length 123	
17	42	30.9%	42	DB 1	Length 227	
18	41	30.5%	41	DB 1	Length 1245	
19	41	30.1%	41	DB 1	Length 473	
20	41	30.1%	41	DB 1	Length 473	
21	41	30.1%	41	DB 1	Length 607	
22	41	30.1%	41	DB 1	Length 607	
23	41	30.1%	41	DB 1	Length 1013	
24	41	30.1%	41	DB 1	Length 1147	
25	41	30.1%	41	DB 1	Length 1147	
26	41	30.1%	41	DB 1	Length 1147	
27	41	30.1%	41	DB 1	Length 664	
28	41	30.1%	41	DB 1	Length 703	
29	41	30.1%	41	DB 1	Length 635	
30	41	30.1%	41	DB 1	Length 635	
31	40	29.8%	40	DB 1	Length 1773	
32	40	29.8%	40	DB 1	Length 1655	
33	40	29.8%	40	DB 1	Length 1655	
34	40	29.4%	40	DB 1	Length 590	
35	40	29.4%	40	DB 1	Length 379	
36	40	29.4%	40	DB 1	Length 1996	
37	40	29.4%	40	DB 1	Length 479	
38	40	29.4%	40	DB 1	Length 613	
39	40	29.4%	40	DB 1	Length 346	





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RX MEDLINE: 94102744.
RA YAMAWA M., YAMAI S., ARIKAWA A.
R1 "Analysis of products of the Escherichia coli genome genes and
R2 translation of their expressions in an applicable procedure for genomic
R3 analysis of other microorganisms."
R4 Biosci. Biotechnol. Biochem. 64:117-129(1994).
R5 1. SIMILARITY: Signal. To: H. HIRATAKEHARA H1171.1.
R6
R7 This SWISS-PROT entry is copyright. It is produced through a collaboration
R8 between the Swiss Institute of Bioinformatics and the EMBL outstation.
R9 The European Bioinformatics Institute. There are no restrictions on its
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R12 entities requires a license agreement (see http://www.ebi.ac.uk/infocentre/
R13 or send an email to license@ebi.ac.uk).
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DR PSSP: P08254; ISLN.
DR GYM: 602541.
DR PROSITE: PS00024; HEMOPEXIN: 1.
DR PROSITE: PS00142; ZINC_PROTEASE: 1.
DR PROSITE: PS00546; CYSTEINE_SWITCH: 1.
DR PFAM: PF00445; hemopexin: 4.
DR PFAM: PF00413; peptidase_M10: 1.
DR Transmembrane. Metalloprotease; zinc; zymogen; calcium; signal;
KM Transmembrane.
FT SIGNAL 1 41
FT PROPEP 42 131
FT CHAIN 132 659
FT TRANS 142 925
FT TRANS 926 140
FT DOMAIN 647 659
FT DOMAIN 109 116
FT DOMAIN 267 559
FT METAL 268 269
FT ACT_SITE 263 263
FT METAL 269 269
FT CARBOHYD 150 150
FT DISULFID 470 559
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Query Match 33.1% Score 45; DB 1; Length 669;
Best Local Similarity 50.0% Prod. No. 17;
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

OY 7 LQMPGPKHLVDEL 22
1:1 1:1 1:1 1:1
DR 542 LQMPGPKHLVDEL 557

RESULT 8
V076_HUMAN STANDARD; PRT; 1998 AA.
AC Q1499;
DI 01-NOV-1997 (Rel. 35, Created)
DI 01-NOV-1997 (Rel. 35, Last sequence update)
DI 01-NOV-1997 (Rel. 35, Last annotation update)
DE HYPOHEMIC PROLEIN KIAA0076 (db00345).
GN KIAA0076.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
[1]
R1 SEQUENCE FROM N.A.
R2 TISSUE-BONE MARROW.
R3 MEDLINE: 9601396.
R4 NAKAMURA N., NAKASE T., MIYATA N., SAZUKA T., TANAKA A., SATO S.,
R5 SERI N., KAWABAYASHI Y., ISHIKAWA K.-I., TABATA S.,
R6 "Prediction of the coding sequences of unidentified human genes. II.
R7 The coding sequences of 40 new genes (K14A004-K14A009) deduced by
R8 analysis of cDNA clones from human cell line K14."
R9 DNA Res. 1:223-229(1994).
R10
R11 This SWISS-PROT entry is copyright. It is produced through a collaboration
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